

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVYLL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10

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Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNIVTP RTPPP	1220	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table XIX

p53 DR Super Motif Peptides with Binding Data												
Core Sequence	Core SeqID Num	Exemplary Sequence	Position	Exemplary SeqID Num	DR1	DR2w β 1	DR2w β 2	DR3	DR4w4	DR4w5	DR5w1	DR5w12
VICTYSPAL	1123	AKSVTCTYSPALNKW	1057	119								
LKDAQAGKE	1124	AELKDQAQGKEPGG	1058	347								
VAPAPAAPT	1125	APPVAPAPAAAPTAA	1059	70								
MPEAAPPVA	1126	APRMPEAAPP/APAP	1060	63								
WPLSSSVPS	1127	APSWSLSSVPSQKT	1061	88								
IHYNNMCMNS	1128	CTTHHYNMCMNSCM	1062	229								
YFTLQIRGR	1129	DGEVFTLQLQRGRERF	1063	324	0.0400					-0.0027		
LSPDDEIEQW	1130	DLMILSPDDEIEQWFTE	1064	42					0.0150			
VEPPLSQTET	1131	DPSVEPPLSQTETPSD	1065	7						0.0039		
LRVEYLDDR	1132	EGNURVEYLDDRNTF	1066	198						0.0039		
VLSPLPSSA	1133	ENNVSLSPLSQAMDD	1067	28								
LAKTCPVQL	1134	FCQLAKTCVQLWVD	1068	134								
LWKLLPENN	1135	FSDLWKLLPENNVL	1069	19								
LGFLLHSGT	1136	GFRLLGFLHSGTAKSV	1070	108							0.2000	
VRAMAIVYKQ	1137	GTRVRAAMAIVYKSOQH	1071	154								
LPPGSTKRA	1138	HHELPPGSTKRALPN	1072	296								
VVPYEPPEV	1139	HSWVVPYEPPEVGSD	1073	214								
YMCNSSCMGG	1140	HYNNMCMNSCMGGMN	1074	233								
WFTEDPGPD	1141	IEQWFTEDPGDEAP	1075	50								
LPNNNTSSSP	1142	KRALPNNTSSSPQPK	1076	305	-0.0005					-0.0027		
LHSGTAKSV	1143	LGFLIHSGTAKSVCT	1077	111								
MFCOLAKTC	1144	LNKMFOLAKTCVQ	1078	130								
LPSQAMDDL	1145	LSPLPSQAMDDLMLS	1079	32								
ITLEDSSGN	1146	LTHTLEDSGNNLLG	1080	252								
MNRRLPILT	1147	MGGGMNRRPILTITL	1081	243	-0.0005					-0.0027		
VYRRCPHIE	1148	MTEVYVRCPHHERCS	1082	169								
LELKDAQAG	1149	NEALELKDAQAGKE	1083	345								
LSPLPSQAM	1150	NNVLISPLPSQAMDDL	1084	29								
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085	47								
VGSDCTTH	1152	PPEVGSDCTTHHYNY	1086	222								
LWVDSTTPPP	1153	PVQLWWVDSTTPPGTR	1087	142								
VDSTTPPGT	1154	QLWVDSTTPPGTRVR	1088	144								
FHSGTIAKS	1155	RJGLFHSGTAKSVTC	1089	110								
FEVRVACP	1156	RNSFEVRCACPGRD	1090	267								
FRHSVVVPPY	1157	RNTRFRHSVVVPPY	1091	209								
LTTLEDS	1158	RPLTITLEDSSEN	1092	249								
ILTTLEDS	1159	RPLTITLEDSGG	1093	248	0.0010					0.0100		
VRVCACPGR	1160	SFEVRVCACPGRDRR	1094	269								
LLGRNSFEV	1161	SGNLIGRNSFEVRC	1095	261								
LNMKMFQCLQA	1162	SPALNKMFCQCLAKTC	1096	127								
MDDMLSPD	1163	SQAMDDMLSPDDIE	1097	37								
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098	94								
VPYEPPEVG	1165	SVVVPPYEPPEVGSDC	1099	215								
LSSSPVPSQK	1166	SWPLSSSPVPSQKTYQ	1100	90								
FRLGFLHS	1167	SYGFRLGFLHSCTAK	1101	106								
LDDRNTFRH	1168	VEYLDDRNTFRHSVV	1102	203								
WVDSTTPPG	1169	VQLWWVDSTTPPGTRV	1103	143								
YEPPEVGSD	1170	VVPPYEPPEVGSDCTT	1104	217								
LPENNVLSP	1171	WKLLPENNVLSP	1105	23								
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106	234								

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Table XIX

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VICVSPAL	1123	AKSVITCTYSPALNKM	1057					
LKDQAQAGKE	1124	ALEKDAQAGKEPGG	1058					
VAPAPAAPT	1125	APPVAPAPAAPTAA	1059					
MPEAAPVVA	1126	APRMPEAAPVVAAP	1060					
WPLSSVPS	1127	APSVPLOSSVPSOKT	1061					
IHYNTMNCNS	1128	CTTHYNHNMCSNCM	1062					
YFTLQLRGR	1129	DGEYFTLQLRGRERF	1063	-0.0018				
LSPDDIEQW	1130	DLMILSPDIEQWFTTE	1064					
VEPPLSQET	1131	DPSVEPPLSQETFSF	1065					
LRYEVYDDR	1132	EGLNRLRVEYLDDRNTF	1066					
VLSPLPSQA	1133	ENNYVLSPLPSOAMDD	1067					
LAKTCPYQL	1134	FCQLAKTCPCVQLWVD	1068					
LWKLLPENN	1135	FSDLWKLPPENNVLV	1069					
LGFLHSGTIA	1136	GFLGFHLHSGTAKSV	1070					
VRAMAIIYKQ	1137	GTRVRAMAIIYKQSQH	1071					
LPGGSTKRA	1138	HHELPPGSTKRALPN	1072					
VVYYEPPEV	1139	HSVVVPVYEPPEVGSD	1073					
YMCNSSCMCG	1140	HYNYNMCMNSSCMGMN	1074					
WFTEDPGPDP	1141	IEQWFTEDPGPDEAP	1075					
IPNNNTSSSP	1142	KRALPNNTSSSPQPK	1076	-0.0007				
LHSHTAKSV	1143	LGFLHSGTAKSVTCT	1077					
MFCQLAKTC	1144	LNMKFCQLAKTCPTVQ	1078					
LPSONAMDDL	1145	LSPQAMDDMLMLS	1079					
TLEDSSGN	1146	LTTIILEDSSGNLIG	1080					
MNRRLPILTI	1147	MGGMNRRLPILTHL	1081	-0.0007				
VVRCPHHE	1148	MTEVYRRCPHHERCS	1082					
LELKDAQAG	1149	NEALELKDAQAGKEP	1083					
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084					
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085					
VGSDCTTH	1152	PPEVGSDCDTTHHNY	1086					
LWDIDSTPPP	1153	PWQWLWDSTTPPPGTR	1087					
VIDSTPPP	1154	QLWVWDSTTPPPGTR	1088					
FLHSHTAKS	1155	RJLGFLHSGTAKSVC	1089					
FEVRCACP	1156	RNSFEVRCAACGRD	1090					
FRIISVVVPPY	1157	RNTFRHSVVVPPYEP	1091					
LTTLEEDS	1158	RPLTTLTLEDSSN	1092					
LTTLIED	1159	RPLLTLTLEDSSG	1093					
VRVCACPGR	1160	SFEVRVCACPGRDR	1094					
LLGRNSFEV	1161	SQNLLGRNSFEVRC	1095					
LNKMFCOLA	1162	SPALNKKMFCOLAKTC	1096					
MDDLMLSPD	1163	SOAMDDMLMLSPDIE	1097					
VPSOKTYQG	1164	SSSVPSQSKTYQSYG	1098					
VPYEPPEV	1165	SVVVPYEPPEVGSDC	1099					
LSSVPSSQK	1166	SWPLSSVPSSQKTYQ	1100					
FRLGFLHSG	1167	SYGERLGFELHSCTAK	1101					
LDDRNTRFH	1168	VEYLDDRNTRFHSTV	1102					
WV DSTPPP	1169	VQLWWVWDSTTPPPGTR	1103					
YEPPEVGSD	1170	VVYYEPPEVGSDCIT	1104					
LPENNVLSP	1171	WKLLPENNVLSPS	1105					
MCNSSCMGG	1172	YNYMCMNSSCMGMNR	1106					

Table XXa p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num.	Position	DR1	DR2w β 1	DR2w2R2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSPDDIEQW	1173	DLMLSPPDDEQWQFTE	1107	42							0.0150	
LRVEYLDDR	1174	EGNIRVEYLDQRNTF	1108	198							0.0039	
LSQEFTSDL	1175	EPPLSQEFTSDLWKL	1109	11							-0.0025	
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110	51							-0.0025	
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111	320							-0.0025	
ITLEDSSGN	1178	LTITLIEDSSGNLLG	1112	252							0.0030	
LIPENNVL	1179	LWKLLPENNVLSPLP	1113	22							0.0029	
VGSDCTTIH	1180	PPEVGSDCTTIIHYNY	1114	222							0.0380	
LWV DSTPPP	1181	PVQLWV DSTPPP GTR	1115	142							0.0300	
RVEGNLRLV	1182	QHLIRVEGNLRLVEYL	1116	192							0.0960	
MFRELNEAL	1183	RDEMFLRELNEALELK	1117	337							0.0052	
YLDDRNTR	1184	RVEYLD DRNTR HSV	1118	202							0.1800	
VPYERPEVG	1185	SVVVV PYEPPEVG SDC	1119	215							-0.0025	

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Table XXa

p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	DR6w19 SeqID Num	DR7	DR8w2	DR9	DRw53
LSPDDIEQW	1173	DLMISPDIDIEQWFT	1107				
LRYVEYLDDR	1174	EGNLRVEYLDDRNTF	1108				
LSOETFSSDL	1175	EPPLSQETFSSDLWKL	1109				
FTEDPGPDE	1176	EQWFTEDPGDFDEAPR	1110				
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111				
ITLEDSSGN	1178	LTTITLEDSSGNLLG	1112				
LLPENNVL	1179	LWKLLPENNVLSPLP	1113				
VGSDCTTIH	1180	PPEYGSDCTTHHYNY	1114				
LWWWDSTPPP	1181	PVQLWWWDSTPPPGR	1115				
IRVEGNLRLV	1182	QHURVEGNLRLVEYL	1116				
MFRELNEAL	1183	RFEMFRELNEALELK	1117				
YLDDRNTFR	1184	RVEYLDDRNTFRHSV	1118				
VPYEPPEVG	1185	SVVVVYEPPEVGSDC	1119				

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Table XXb p53 DR 3b Motif Peptides with Binding Data

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Core Sequence	Core SeqID Num	Exemplary Sequence	Table XXb p53 DR 3b Motif Peptides with Binding Data				
			DR6w19	DR7	DR8w2	DR9	DRw33
FTLQIRGRE	1186	GEVTTLOIRGRERFE	1120				
VEGNLRVEY	1187	LIRVEGNLRVEYLDD		1121			
YKQSQHMTE	1188	MAIYKQSQHMTEVVR			1122		

Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM
p53.24	9	KLLPENNVL	1224	313
p53.24V9	9	KLLPENNVV	1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78
p53.65	10	RMPEAAPPVA	1230	78
p53.65L2V10	10	RLPEAAPPVV	1231	143
p53.65M2V10	10	RMPEAAPPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGRFL	1235	1786
p53.101L2V11	11	KLYQGSYGRFV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWV	1252	725
p53.139L2	9	KLCPVQLWV	1253	122
p53.139L2B3	9	KLBPVQLWV	1254	46
p53.149	9	STPPPGTRV	1255	909
p53.149M2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
p53.164	9	KQSQHMTEV	1258	500
p53.164L2	9	KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNYM	1262	278
p53.229L2V9	9	CLTIHYNYV	1263	263
p53.229B1L2V9	9	BLTIHYNYV	1264	116
p53.236	8	YMCNSSCM	1265	4546
p53.236L2M8	8	YLCNSSCV	1266	--
p53.236	11	YMCNSSCMGGM	1267	667
p53.236L2M11	11	YLCNSSCMGGV	1268	22
p53.255	11	ITLEDSSGNLL	1269	1563
p53.255L2V11	11	ILLEDSSGNLV	1270	33
p53.256	10	TLEDSSGNLL	1271	1667
p53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYNY	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5

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Table XXIB A03 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0301 nM</u>	<u>A*1101 nM</u>	<u>A*3101 nM</u>	<u>A*3301 nM</u>	<u>A*6801 nM</u>	<u>A3 XRN</u>
1371.14	10	KVYQGSYGF	1278	p53.101.V2	37.9	61.9	72	10000	40	4
1371.15	10	KVYQGSYGFK	1279	p53.101.V2K10	33.3	9.2	138.5	-72500	38.1	4
1371.16	9	BVYSPALNK	1280	p53.124.B1V2	15.7	12.8	439	22307.7	500	4
1371.17	9	BVYSPALNR	1281	p53.124.B1V2R9	25	8.3	33.3	85.3	14.8	5
1371.18	8	KVFBQLAK	1282	p53.132.V2B4	846.2	461.5	7500	-72500	8888.9	1
1371.2	11	GVRVRA MaiYK	1283	p53.154.V2	57.9	136.4	418.6	-72500	133333.3	3
1371.22	9	RVRAMA MaiYR	1284	p53.156.R9	40.7	1666.7	8.6	-72500	666.7	3
1371.24	9	SVBMGGMNIK	1285	p53.240.V2B3K9	12.5	17.1	9000	-72500	29.6	3
1371.25	10	SVBMGGMNRIK	1286	p53.240.V2B3K10	100	75	-36000	-72500	17	3
1371.26	9	SVBMGGMNR	1287	p53.240.V2B3	161.8	95.2	120	852.9	11.1	4
1371.27	10	SVBMGGMNRR	1288	p53.240.V2B3	1000	25	620.7	805.6	11.4	2
1371.31	11	RVBABPGDRDK	1289	p53.273.B3B5K11	314.3	200	4615.4	-72500	2500	2
1371.32	11	SVSRHKKLMFK	1290	p53.376.V2	33.3	54.5	295.1	18125	1509.4	3
1371.33	11	SVSRHKKLMFR	1291	p53.376.V2R11	196.4	2857.1	183.7	1381	500	3

Table XXIIC A02 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0201 nM</u>	<u>A*0202 nM</u>	<u>A*0203 nM</u>	<u>A*0206 nM</u>	<u>A*6802 nM</u>	<u>A2 XRN</u>
27.0068	9	KMF CQLAKT	1292	p53 132	505.1	14.3	19.6	92.5	-40000	3
39.0074	9	LLGRD SFEV	1293	mp53.261	41.7					
44.0003	9	LLGRD SFEV	1294	mp53.261	27.8					
1317.22	9	ALN KMF CQL	1295	p53.129	735.3	390.9	18.5	72.5		
1317.23	9	KMF CQLAKT	1296	p53.132	333.3	33.1	17.5	105.7	-80000	3
1324.08	9	KQS QHM TEV	1297	p53.164	500	130.3	169.5	284.6	-80000	4
1329.04	9	CTTI HYNYM	1298	p53.229	277.8	286.7	2564.1	560.6	181.8	3
1329.07	9	KLP PENN VL	1299	p53.24	312.5	1954.5	12500	1193.5	-80000	1
1329.09	10	FLHS GTAK SV	1300	p53.113	357.1	179.2	14.5	4625	80000	3

All
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Table XXIID A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303	p53.102	100
52.0104	10	TYSPALNKM F	1304	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKL F	1309	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0096	10	TYQGSYGFRF	1311	p53.102.F10	30



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TABLE XXII E B07 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>B*0702 nM</u>	<u>B*3501 nM</u>	<u>B*5101 nM</u>	<u>B*5301 nM</u>	<u>B*5401 nM</u>	<u>B7 XRN</u>
48.0055	8	FPALNKM F	1312	p53.127.F1	0.025	3000	18333.3	6200	3846.2	1
48.0234	11	FPALNKMFCQL	1313	p53.127.F1	0.052	2482.8	5500	7750	500	2
48.0123	9	FPGTRVRAI	1314	p53.152.F1	1.1	-36000	662.7	23250	2439	1
48.0196	10	FPPGSTKRAL	1315	p53	0.79	-24000	6111.1	-23250	-20000	1
48.0127	9	FPQPKKKP I	1316	p53	0.61	-36000	-55000	-31000	16666.7	1
48.0128	9	FPQPKKKPL	1317	p53	2.3	-36000	-55000	-31000	-100000	1

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Connie
Table XXIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 Crossbound	No. A2 Alleles	CTL CTL	CTL Wild-type	CTL CTL Tumor
p53.135	9	CQLA K TCPV	1318	208	43.0	143.0	90.0	-- ²	4	--	1/4	0/4
p53.69	8	AAPPVAPA	1319	5000	1536	1177	1233	4706	0	--	1/4	0/4
p53.69L2V8	8	ALPPVAPV	1320	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNK M FCQL	1321	735	391	19	73	-- ²	3	--	4	0/1
p53.129V9	9	ALNK M FCQV	1322	75	165	7.7	15	--	4	--	4	0/1
p53.129B7V9	9	ALNK M FBQV	1323	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMF C QLAKT	1324	333	33	18	106	--	4	--	4	0/2
p53.132V9	9	KMF C QLAKV	1325	33	8.4	7.7	15	--	4	--	4	0/2
p53.132B4V9	9	KMF B QLAKV	1326	125	13	9.1	37	8889	4	--	5/5	0/4
p53.132L2V9	9	KLF C QLAKV	1327	98	3.6	3.4	9.5	1270	4	--	2/3	0/3
p53.139	9	KTCPVQLWV	1328	725	606	217	15	--	2	--	2	0/2
p53.139L2	9	KLCPVQLWV	1329	122	239	29	23	--	4	--	4	0/2
p53.139L2B3	9	KLBPVQLWV	1330	45	29	19	31	--	4	--	4	0/4
p53.149	9	STPPP G TRV	1331	909	1162	1031	--	129	1	--	3/4	2/3
p53.149L2	9	STPPP G TRV	1332	122	226	13	9250	140	4	--	2/5	2/3
p53.149M2	9	SMPPP G TRV	1333	172	215	13	425	667	4	--	3/4	2/3
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	--	1	--	2/4	2/4
p53.216L2	10	VLVPYEPPEV	1335	89	391	71	2056	--	3	--	1/1	1/1
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	6667	0	--	1/3	0/3
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		SEQ ID NO:
				Source	Sequence	
Human	A1	A*0101	Steinlin	Hu. J chain	102-110	1338
	A2	A*0201	JY	HBVc	18-27 F6->Y	1339
	A2	A*0202	P815 (transfected)	HBVc	18-27 F6->Y	1340
	A2	A*0203	FUN	HBVc	18-27 F6->Y	1341
	A2	A*0206	CLA	HBVc	18-27 F6->Y	1342
	A2	A*0207	'21.221 (transfected	HBVc	18-27 F6->Y	1343
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	1344
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	1345
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	1346
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	1347
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	1348
	A28/68	A*6801	C1R	HBVc	141-151 T7->Y	1349
	A28/68	A*6802	AMAI	HBV pol	646-654 C4->A	1350
	B7	B*0702	Gm3107	A2 signal seq.	5-13 (L7->Y)	1351
	B8	B*0801	Steinlin	IV gp	586-593 Y1->F, Q5->	1352
	B27	B*2705	LG2	R 60s	FRYNGLIHR	1353
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	PPFKYAAAF	1354
	B35	B*3502	TISI	non-natural (B35CON2)	PPFKYAAAF	1355
	B35	B*3503	EHM	non-natural (B35CON2)	PPFKYAAAF	1356
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	1357
	B51		KAS116	non-natural (B35CON2)	PPFKYAAAF	1358
	B53	B*5301	AMAI	non-natural (B35CON2)	PPFKYAAAF	1359
	B54	B*5401	KT3	non-natural (B35CON2)	PPFKYAAAF	1360
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	1361
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDDGNVL	1362
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDDGNVL	1363
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	1364
	K ^b		EL4	VSV NP 52-59	RGYVFQGL	1365
	D ^d		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	1366
	K ^d		P815	non-natural (KdCON1)	KFNPMMKTYI	1367

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

L ^d	P815	HBVs 28-39	IPQSLSYWTSL	1368
B. Class II binding assays				
Species	Antigen	Allele	Cell line	Source
Human	DR1	DRB1*0101	LG2	HA Y307-319
	DR2	DRB1*1501	L466.1	MBP 88-102Y
	DR2	DRB1*1601	L242.5	non-natural (760.16)
	DR3	DRB1*0301	MAT	MT 65kD Y3-13
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)
	DR4w10	DRB1*0402	YAR	non-natural (717.10)
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)
	DR4w15	DRB1*0405	KT3	non-natural (717.01)
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843
	DR8	DRB1*0802	OLL	Tet. tox. 830-843
	DR8	DRB1*0803	LJY	Tet. tox. 830-843
	DR9	DRB1*0901	HID	Tet. tox. 830-843
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843
	DR12	DRB1*1201	Herluf	unknown eluted peptide
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843
	DR51	DRB5*0201	L255.1	HA 307-319
	DR52	DRB3*0101	MAT	Tet. tox. 830-843
	DR53	DRB4*0101	L257.6	non-natural (717.91)
	DQ3.1	Q ₁ A1*0301/DQB1*0301	PF	non-natural (RoIV)
Mouse	IA ^b		DB27.4	non-natural (RoIV)
	IA ^d		A20	non-natural (RoIV)
	IA ^k		CH-12	HEL 46-61
	IA ^s		LS102.9	non-natural (RoIV)
	IA ^u		91.7	non-natural (RoIV)
	IE ^d		A20	Lambda repressor 12-26
	IE ^k		CH-12	Lambda repressor 12-26
				YAHAAHAAHAAHAAHAA
				1389
				YAHAAHAAHAAHAAHAA
				1390
				YNTDGSTDYGILQINSR
				1391
				YAHAAHAAHAAHAAHAA
				1392
				YAHAAHAAHAAHAAHAA
				1393
				YLEDARRKKAIYEKKK
				1394
				YLEDARRKKAIYEKKK
				1395

a7

Table XXVI. Crossbinding of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201			A*0202			A*0203			A*0206			A*6802			No. A2 Alleles	Crossbound
				nM	nM	nM	nM	nM												
p53.24	9	KLLPENNVL	1396	313	1955	--	1194	--	--	1194	--	--	1194	--	--	--	--	1		
p53.25	11	LLPENNVL SPL	1397	19	6.2	4.5	12	1702	1702	1702	1702	1702	1702	1702	1702	1702	1702	4		
p53.65	10	RMPEAAPPVA	1398	78	102	13	841	--	--	841	--	--	841	--	--	--	--	3		
p53.65	9	RMPEAAPPV	1399	119	23	22	70	--	--	70	--	--	70	--	--	--	--	4		
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	--	--	4625	--	--	4625	--	--	--	--	3		
p53.132	9	KMFCQLAKT	1401	333	33	18	106	--	--	106	--	--	106	--	--	--	--	4		
p53.135	9	CQLAKTCPV	1402	208	43	143	90	--	--	90	--	--	90	--	--	--	--	4		
p53.136	8	QLAKTCPV	1403	455	--	100	2643	1067	1067	2643	1067	1067	2643	1067	1067	1067	1067	2		
p53.164	9	KQSQHMTEV	1404	500	130	170	285	--	--	285	--	--	285	--	--	--	--	4		
p53.187	11	GLAPPQHLIRV	1405	79	39	11	55	--	--	55	--	--	55	--	--	--	--	4		
p53.193	11	HILRVEGNLRV	1406	385	1387	83	1194	1778	1778	1194	1778	1778	1194	1778	1778	1778	1778	2		
p53.229	9	CTTHYNYM	1407	278	287	2564	561	--	--	561	--	--	561	--	--	--	--	4		
p53.263	10	NLLGRNSFEV	1408	217	--	2500	881	--	--	881	--	--	881	--	--	--	--	3		
p53.264	9	LLGRNSFEV	1409	85	358	37	206	--	--	206	--	--	206	--	--	--	--	4		

-- indicates binding affinity = 10,000nM.

A7
Cont.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ ID NO:	A*0201	A*0202	A*0203	A*0206	A*6802	No. A2 CTL	CTL Wild-type ¹	Tumor
		nM	nM	nM	nM	nM	Crossbound			
p53.135	CQLAKTCPV	1410	208	43	143	90	-- ²	4	1/4	0/1

1) Number of donors yielding a positive response/total tested.
2) -- indicates binding affinity =10,000nM.

cont'd
Table XXVIII. Crossbinding of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	Crossbound
p53.69	8	AAPPVAPA	1411	5000	1536	1177	1233	4706	0	
p53.69L2V8	8	ALPPVAPV	1412	217	7167	500	285	67	4	
p53.101	11	KTYQGSYGFRL	1413	1786	896	--	514	615	0	
p53.101L2V1	11	KLYQGSYGFRLV	1414	81	48	24	116	--	4	
p53.129	9	ALNKMFCQL	1415	735	391	19	73	--	3	
p53.129V9	9	ALNKMFCQV	1416	75	165	7.7	15	--	4	
p53.129B7V9	9	ALNKMFBQV	1417	192	391	23	49	--	4	
p53.129	10	ALNKMFCQLA	1418	1316	1075	71	4625	--	1	
p53.129V10	10	ALNKMFCQLV	1419	217	287	71	7400	--	3	
p53.132	9	KMFCQLAKT	1420	333	33	18	106	--	4	
p53.132V9	9	KMFCQLAKV	1421	33	8.4	7.7	15	--	4	
p53.132B4V9	9	KMFBQLAKV	1422	125	13	9.1	37	8889	4	
p53.132L2V9	9	KLFCQLAKV	1423	98	3.6	3.4	10	1270	4	
p53.135	9	CQLAKTCPV	1424	208	43	143	90	--	4	
p53.135L2	9	CLAKTCPV	1425	125	506	67	370	--	3	
p53.135B1B7	9	BQLAKTBPV	1426	102	71	15	67	--	4	
p53.135B1L2I	9	BLAKTBPV	1427	46	119	7.7	64	--	4	
p53.139	9	KTCPVQLWW	1428	725	606	217	15	--	2	
p53.139L2	9	KLCPVQLWW	1429	122	239	29	23	--	4	
p53.139L2B3	9	KLBPVQLWW	1430	46	29	19	31	--	4	
p53.149	9	STPPPGTRV	1431	909	1162	1031	--	129	1	
p53.149M2	9	SMPPPGBT	1432	172	215	13	425	667	4	
p53.149L2	9	SLPPPGBT	1433	122	226	13	9250	140	4	
p53.164	9	KQSQHMTEV	1434	500	130	170	285	--	4	
p53.164L2	9	KLSQHMTEV	1435	122	94	35	46	--	4	
p53.216	10	VVVPYEPPEV	1436	617	1870	455	1194	--	1	
p53.216L2	10	VLPVYEPPEV	1437	89	391	71	2056	--	3	
p53.236	11	YMCNSSCMGGM	1438	667	391	67	974	5333	2	
p53.236L2M1	11	YLCNSSCMGGV	1439	22	13	3.6	18	1569	4	
p53.255	11	ITLEDSSGNLL	1440	1563	1265	2857	507	6667	0	
p53.255L2V1	11	ILLEDSSGNLV	1441	33	123	71	206	--	4	

-- indicates binding affinity = 10,000nM.

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*6802 nM	No. A2 Alleles	CTL Crossbound	CTL Peptide ¹	CTL Wild-type	CTL Tumor
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1443	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1444	735	391	19	73	-- ²	3			
p53.129V9	9	ALNKMFCQV	1445	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1446	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFQQLAKT	1447	333	33	18	106	--	4			
p53.132V9	9	KMFQQLAKV	1448	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFQQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFQQLAKV	1450	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWW	1451	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWW	1452	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWW	1453	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPPTTRV	1454	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPPTRV	1455	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPPPTRV	1456	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1458	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

Table XXX. DR supertype primary binding

*A7
cont.*

Peptide	DR147		SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross-binding
	Algo	Sum						
39.0307	2	GFR LGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	L N K M F C Q L A K T C P V Q	1462	P53.130	20	804	167	3
39.0309	2	M G G M N R R P I L T I I T L	1463	P53.243	--	--	--	0
39.0310	2	R R P I L T I I T L E D S S G	1464	P53.248	5000	4500	--	0
39.0311	2	K R A L P N N T S S S P Q P K	1465	P53.305	--	--	--	0
39.0312	2	D G E Y F T L Q I R G R E R F	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

A7
cont.

Table XXXI. DR supertype cross-binding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR5w1 9 nM	DR8w1 1 nM	DR8w2 nM	DR147 Binding (5/8)	Broad Binding
39.0307	GFRLLGFLHSGTAKSV	1467	p53.108	2.6	5.4	89	253	167	76	100	29	3	8
39.0308	LNKMFQQLAKTCPV	1468	p53.130	20	804	167	5688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.

Table XXXII. DR3 binding

Peptide	Sequence	iEQ ID NC	Source	DR3 nM
39.0409	EPPLSQETFSDLWKL	1469	p53.11	--
39.0410	LWKLLPENNVLSPLP	1470	p53.22	--
39.0411	DLMMLSPDDIEQWFTE	1471	p53.42	--
39.0412	EQWFTEDPGPDEAPR	1472	p53.51	--
39.0413	PVQLWVDSTPPPGTR	1473	p53.142	--
39.0414	MAIYKQSQHMTEVVR	1474	p53.160	--
39.0415	QHLIRVEGNLRVEYL	1475	p53.192	3125
39.0416	LIRVEGNLRVEYLDD	1476	p53.194	3226
39.0417	EGNLRVEYLDLDRNTF	1477	p53.198	--
39.0418	RVEYLDDRNTFRHSV	1478	p53.202	1667
39.0419	SVVVVPYEPPEVGSDC	1479	p53.215	--
39.0420	PPEVGSDCTTIHYNY	1480	p53.222	7895
39.0421	LTIITLEDSSGNLLG	1481	p53.252	--
39.0422	KKPLDGEGYFTLQIRG	1482	p53.320	--
39.0423	GEYFTLQIRGRERFE	1483	p53.325	--
39.0424	RFEMFRELNEALELK	1484	p53.337	--

-- indicates binding affinity =10,000nM.

07
Conf.

Table XXXIII. HTL candidate peptides

Peptide	Sequence	SEQ ID Source NO:	DR1	DR4w	DR7	DR3	DR2w	DR2w	DR5w	DR8w	DR14
			nM	nM	nM	2 β1 nM	2 β2 9 nM	1 1 nM	2 nM	7	Broad Binding (5/8)
39.0307	GFRLLGFLHSGTAKSV	1485 p53.108	2.6	5.4	89	--	253	167	76	100	29
39.0308	LNKMFQCLAKTCPVQ	1486 p53.130	20	804	167	--	5688	541	365	2500	1531

-- indicates binding affinity = 10,000nM.

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLEL	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVYLL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10

101

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNIVTP RTPPP	1220	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Core Sequence	Core SeqID Num	Exemplary Sequence	Position SeqID Num	P53 DR Super Motif Peptides with Binding Data
				Exemplary Position SeqID Num
				DR1 DR2w β 1 DR2w β 2 DR3 DR4w4 DR4w15 DR5w11 DR5w12
VTCTYSPAL	1123	/AKSVTCTYSPALNKM	1057	119
LKDAQAGKE	1124	/ALELKDAQAGKEPGG	1058	347
VAPAAAPT	1125	APPVAPAAAPTAA	1059	70
MPEAAPPVA	1126	APRMPEAAPPVAAP	1060	63
WPLSSVPS	1127	APSWPLOSSVPSQKT	1061	88
IHYNNMCSNS	1128	CTTHHYNMCMNSCM	1062	229
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063	324
LSPDDIEQW	1130	DLMSPDDIEQWFTIE	1064	42
VEPPLSQET	1131	DPSVEPPLSQETFSD	1065	7
LRVEYLDTR	1132	EGNLRLVEYLDTRNTF	1066	198
VLSPLPSQA	1133	ENNVLSPLPSQAAMD	1067	28
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068	134
LWKLLPENLN	1135	FSDLWKLIPENNVLSS	1069	19
LGFLHSGTIA	1136	GFLGLFLHSGTIAKSV.	1070	108
VRAMAIIYKQ	1137	GTRVRAAMAIYKQSQH	1071	154
LPPGSTKRA	1138	HHELPGGSTKRALPN	1072	296
VVPYEEPVV	1139	HSAVAVPYEEPEVQSD	1073	214
YMCNSSCMG	1140	HYNMCCNSCMGGMN	1074	233
WFEDPQPD	1141	IEQWFEDPQPDDEAP	1075	50
LPNNNTSSSP	1142	KRALPNNTSSSPQPK	1076	305
LHSGTAKSV	1143	LGFLHSGTAKSVGT	1077	111
MFCOLAKTC	1144	LNMKFCOLAKTCVQ	1078	130
LPSQAMDDL	1145	LSPLPSQAMDDLMLSL	1079	32
ITLEDSSGN	1146	LTTIITLEDSSGNLLG	1080	252
MNRRPILTI	1147	MGGMNRRPILTIUL	1081	243
VVRRCPHIE	1148	MTEVYVRRCPHHERCS	1082	169
LELKDQAQG	1149	NEALELKDAQAGKEP	1083	345
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084	29
IEQWFETDP	1151	PDDIEQWFETDPGPDI	1085	47
VGSDDCTTH	1152	PPEEVGSDCTTHIINYV	1086	222
LWVDSSTPPP	1153	PVQLWVDSSTPPPCTR	1087	142
VDSTTPPGT	1154	QLWVDSSTPPPCTRVR	1088	144
FEVRYCACP	1155	RJLGFHLHSGTAKSVTC	1089	110
FRHSVVVPY	1156	RNSFEVRYCACPGRD	1090	267
LTTITLEDS	1157	RNTFRHSVVVPYEP	1091	209
LTTITLED	1158	RPLLTITLEDSGN	1092	249
FLRSGTAKS	1159	RRPILTITILEDSSG	1093	248
FEVYCACPGR	1160	SFEVYCACPGRDRR	1094	269
LLGRNSFEV	1161	SGNLLGRNSFEV	1095	261
LNKMFQCLA	1162	SPALNKMFCOLAKTC	1096	127
MDDIMLSPD	1163	SQAMDDMLMSPDDE	1097	37
VPSQKTYQG	1164	SSSYPSQKTYQGSGY	1098	94
VPYEPEPEVG	1165	SVAVVYEPFEPVGSDC	1099	215
LSSVPSQK	1166	SWPLSSVPSQKTYQ	1100	90
FRLGFHLSG	1167	SYGFLRLGFHLHSGTAK	1101	106
LDDRNTFRH	1168	VEYLDDDRNTFRHSVY	1102	203
WWDSTTPPG	1169	VQLWWWDSTTPPGTRV	1103	143
YEPPEPEVG	1170	VVYEPPEPEVGSDCTT	1104	217
LPENNVLSP	1171	WLPLPENNVLSPPLPS	1105	23
MCNSSCMG	1172	YNYMCNSSCMGGMNR	1106	234

a. DRw53

no human peptide

each position

Table XIX

Core Sequence	Core SeqID Num	B53 DR Super Motif Peptides with Binding Data						DRw53
		Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	
VICTYSAL	1123	AKSVTCTYSPAINK	1057					
LKDQAQKE	1124	ALEKDAQAGKEPGG	1058					
VAPAPAAPT	1125	APPVAPAPAAPTAAP	1059					
MPEAAPPVA	1126	APSWPAAAPPVAPAP	1060					
WPLSSSVPS	1127	APSWPLSSSVPSQKT	1061					
HYNMCMNS	1128	CTTHYHNMCMNSCM	1062					
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063					
LSPDIEQW	1130	DLMLSPDIEQWITE	1064					
VEPPLSQET	1131	DPSVEPPLSQETFSF	1065					
LRVEYLDDR	1132	EGNLRLVEYLDDRNFT	1066					
VLSPFLPSQA	1133	ENNVLSPLSQAMDD	1067					
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068					
LWKLLPENN	1135	FSDLWKLLPENNKL	1069					
LGFELHSFTA	1136	GFRLGFLHSFTAKSV	1070					
VRAMAIAKYQ	1137	GTRVAMAIAKYQSQHQH	1071					
LPPGSTKRA	1138	HHELPFGSTKRALPN	1072					
VVPPYEPEPV	1139	HSVVPYEPEPVGSDF	1073					
YMCNNSCMG	1140	HYNYNCNNSCMGGMN	1074					
WFTEDPGPD	1141	IEQWFTEDPGPDEAP	1075					
LPNTNTSSP	1142	KRALPNNTNTSSPQPK	1076					
IHSGTAKSV	1143	LGFELHSFTAKSVCT	1077					
MF-COLAKTC	1144	LNMKFCQLAKTCPVQ	1078					
LPSQAMDDL	1145	LSPPLSQAMDDLMLS	1079					
ITLEDSSGN	1146	LTHITLEDSSGNLLG	1080					
MNRRLPIL	1147	MGGGMNRRLPILTLI	1081					
VYRRCPHHE	1148	MTEVVRCCPHHERCS	1082					
LELKDAQAG	1149	NEALELKDAQAGKEP	1083					
ISPLPSQAM	1150	NNVLSPLSQAMDDLL	1084					
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085					
YGSDCTTH	1152	PVEVGSDCTTHHYN	1086					
LWDSTTPP	1153	PVQLWWDSTTPPPGTR	1087					
YDSTTPPPGT	1154	QLWWDSTTPPPGTR	1088					
FHSGTAKS	1155	RLGFLHSFTAKSVTC	1089					
FEVRVCACP	1156	RNSFEVRVCACPGRDR	1090					
FRHSVVVPY	1157	RNTFRHSVVVPYEP	1091					
LTHITLEDS	1158	RPLILTHITLEDSGN	1092					
ILTHITLED	1159	RRPLILTHITLEDSG	1093					
VPSQKTYQG	1160	SFVRVCACPGRDR	1094					
VPEPPEVY	1161	SIGNLGRNSFEVRVC	1095					
LLGRNSFEV	1162	SPALNKMFCQLAKTC	1096					
LNMKFCQLA	1163	SQAMDDLMSPDDE	1097					
MDDLMSPD	1164	SSSVPSOKTYQGSYGY	1098					
VPSQKTYQG	1165	SVVVPYEPEPVGSDC	1099					
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100					
FRLGFLHSG	1167	SYGRFLGFLHSGTTAK	1101					
LDDRNTFRH	1168	VEYLDDRNTFRHSVV	1102					
WVDSTTPPG	1169	VQLWWDSTTPPPGTR	1103					
YEPPEPVEVGS	1170	VYPPPEPVEVGSDCTT	1104					
LPENNVLSP	1171	WKLLPENNVLSP	1105					
MCNSSCMGG	1172	YNYMCNNSCMCGMNR	1106					

Table XXXa p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w5	DR5w11	DR5w12
LSPDDIEQW	1173	DLMILSPDIDIEQWFTE	1107	42							0.0150	
I RVEYLDDR	1174	EGLMLRVEYLDDRNTF	1108	198							0.0039	
LSQETFSSDL	1175	EPLLSQETFSSDLWKL	1109	11							-0.0025	
FTEDPGPDE	1176	EQWFTEIDPGPDEAPR	1110	51							-0.0025	
LDGEYFTLQ	1177	KKPLDGEGFTLQIRG	1111	320							-0.0025	
ITLEDSSGN	1178	LTTITLEDDSGNLLG	1112	252							0.0030	
LLPENNYLS	1179	LWKLLPPENNVLSPLP	1113	22							0.0029	
VGSDCCTTH	1180	PPEVGSDCTTHHYNY	1114	222							0.0380	
I WVDSTTPP	1181	PVQLWWVDSITPPPGTR	1115	142							0.0300	
I RVEGNLRV	1182	QHLIRVEGNLRVEYL	1116	192							0.0960	
MFRELNEAL	1183	RFFEMFRELNEALELK	1117	337							0.0052	
YLDDRNTFR	1184	RVEYLDDDRNTFRHSV	1118	202							0.1180	
V PYEPPEVGV	1185	SVVVVPYEPPEVGSDC	1119	215							-0.0025	

Table XXa

p53 DR-3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	DR6w19 SeqID Num	DR7	DR8w2	DR9	DRw53
LSPDDIEQW	1173	DLMSPDDIEQWFT	1107				
I RVEYLDDR	1174	EGLNLRVEYLDDRNTF	1108				
I S Q E T F S D L	1175	EPPLSQETFSDLWKL	1109				
F T E D P G P D E	1176	EQWFTEDPGPDEAPR	1110				
I D G E Y F T L O	1177	KKPLDGEYFTLQIRG	1111				
I T L E D S S G N	1178	LTTLEDSSGNLLG	1112				
I I L P E N N V L S	1179	LWKLLPENNVLSPLP	1113				
V G S D C T T H	1180	PPEVGSDCTTHNY	1114				
L W V D S T P P P	1181	PVQLWWDSTPPPQTR	1115				
I R V E G N L R V	1182	QHLRVEGNLRVEYL	1116				
M F R E L N E A L K	1183	RFEMFRELNEALELK	1117				
Y L D D R N T F R	1184	RVEYLDDRNTFRHSV	1118				
V P Y E P P E V G	1185	SVVVVYEPPEVGSDC	1119				

Column
Motif
Data

Table XXb p53 DR 3b Motif Peptides with Binding Data

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTLQIRGRE	1186	GEYFTLQIRGREREE	1120					
VEGNLRVEY	1187	LIRVEGNLRVEYLD	1121					
YKQSQHMTE	1188	MAIYKQSQHMTEVVR	1122					

Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM
p53.24	9	KLLPENNVL	1224	313
p53.24V9	9	KLLPENNVV	1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78
p53.65	10	RMPEAAPPVA	1230	78
p53.65L2V10	10	RLPEAAPPVV	1231	143
p53.65M2V10	10	RMPEAAPPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGFRL	1235	1786
p53.101L2V11	11	KLYQGSYGFRV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWW	1252	725
p53.139L2	9	KLCPVQLWW	1253	122
p53.139L2B3	9	KLBPVQLWW	1254	46
p53.149	9	STPPPGTRV	1255	909
p53.149M2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
p53.164	9	KQSQHMTEV	1258	500
p53.164L2	9	KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNYM	1262	278
p53.229L2V9	9	CLTIHYNYV	1263	263
p53.229B1L2V9	9	BLTIHYNYV	1264	116
p53.236	8	YMCNSSCM	1265	4546
p53.236L2M8	8	YLCNSSCV	1266	--
p53.236	11	YMCNSSCMGGM	1267	667
p53.236L2M11	11	YLCNSSCMGGV	1268	22
p53.255	11	ITLEDSSGNLL	1269	1563
p53.255L2V11	11	ILLEDSSGNLV	1270	33
p53.256	10	TLEDSSGNLL	1271	1667
p53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYNY	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5

Table XIIIB A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.14	10	KVYQGSYGFR	1278	p53.101.V2	37.9	61.9	72	10000	40	4
1371.15	10	KVYQGSYGFK	1279	p53.101.V2K10	33.3	9.2	138.5	-72500	38.1	4
1371.16	9	BVYSPALNK	1280	p53.124.B1V2	15.7	12.8	439	22307.7	500	4
1371.17	9	BVYSPALNR	1281	p53.124.B1V2R9	25	8.3	33.3	85.3	14.8	5
1371.18	8	KVFBQLAK	1282	p53.132.V2B4	846.2	461.5	7500	-72500	888.9	1
1371.2	11	GVRVARAMAIYK	1283	p53.154.V2	57.9	136.4	418.6	-72500	13333.3	3
1371.22	9	RVRAMAIYR	1284	p53.156.R9	40.7	1666.7	8.6	138.1	666.7	3
1371.24	9	SVBMGGMINK	1285	p53.240.V2B3K9	12.5	17.1	9000	-72500	29.6	3
1371.25	10	SVBMGGMNRK	1286	p53.240.V2B3K10	100	75	-36000	-72500	17	3
1371.26	9	SVBMGGMNR	1287	p53.240.V2B3	161.8	95.2	120	852.9	11.1	4
1371.27	10	SVBMGGMNRR	1288	p53.240.V2B3	1000	25	620.7	805.6	11.4	2
1371.31	11	RVBABPGRDRK	1289	p53.273.B3B5K11	314.3	200	4615.4	-72500	2500	2
1371.32	11	SVSRHKKLMFK	1290	p53.376.V2	33.3	54.5	295.1	18125	1509.4	3
1371.33	11	SVSRHKKLMFR	1291	p53.376.V2R11	196.4	2857.1	183.7	1381	500	3

① ② ③ ④
⑤ ⑥ ⑦ ⑧

1381

Table XXIIC A02 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0201 nM</u>	<u>A*0202 nM</u>	<u>A*0203 nM</u>	<u>A*0206 nM</u>	<u>A*6802 nM</u>	<u>A2 XRN</u>
27.0068	9	KMFCQLAKT	1292	p53.132	505.1	14.3	19.6	92.5	-40000	3
39.0074	9	LLGRDSFEV	1293	mp53.261	41.7					
44.0003	9	LLGRDSFEV	1294	mp53.261	27.8					
1317.22	9	ALNKMFCQL	1295	p53.129	735.3	390.9	18.5	72.5	-80000	3
1317.23	9	KMFCQLAKT	1296	p53.132	333.3	33.1	17.5	105.7	-80000	3
1324.08	9	KQSQHMTEV	1297	p53.164	500	130.3	169.5	284.6	-80000	4
1329.04	9	CTTIHYNYM	1298	p53.229	277.8	286.7	2564.1	560.6	-80000	4
1329.07	9	KLLPENNVL	1299	p53.24	312.5	1954.5	12500	1193.5	181.8	3
1329.09	10	FLHSGTAKSV	1300	p53.113	357.1	179.2	14.5	4625	-80000	1
									80000	3

add dec 2
10/10/04

Table XXIID A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303	p53.102	100
52.0104	10	TYSPALNKMF	1304	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKLF	1309	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0096	10	TYQGSYGFRF	1311	p53.102.F10	30

TABLE XXIE B07 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>B*0702 nM</u>	<u>B*3501 nM</u>	<u>B*5101 nM</u>	<u>B*5301 nM</u>	<u>B*5401 nM</u>	<u>B7 XRN</u>
48.0055	8	FPALNKM F	1312	p53.127.F1	0.025	3000	183333.3	6200	3846.2	1
48.0234	11	FPALNKMFCQL	1313	p53.127.F1	0.052	2482.8	5500	7750	500	2
48.0123	9	FPGTRVRAI	1314	p53.152.F1	1.1	-36000	662.7	23250	2439	1
48.0196	10	FPPGSTKRAL	1315	p53	0.79	-24000	6111.1	-23250	-20000	1
48.0127	9	FPQPKKKP I	1316	p53	0.61	-36000	-55000	-31000	16666.7	1
48.0128	9	FPQPKKKPL	1317	p53	2.3	-36000	-55000	-31000	-100000	1

141

Table XIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Crossbound	Alleles	CTL	CTL	CTL	Wild-type	Tumor
p53.135	9	CQLAKTCPV	1318	208	43.0	143.0	90.0	-- ²	4	1/4	0/4	0/4	0/4	0/4	0/4
p53.69	8	AAPPVAPA	1319	5000	1536	1177	1233	4706	0	4	2/4	1/3	0/3	0/3	0/3
p53.69L2V8	8	ALPPVAPV	1320	217	7167	500	285	67	4	2/4	1/3	0/3	0/3	0/3	0/3
p53.129	9	ALNKMFCQL	1321	735	391	19	73	-- ²	3	4	0/1	0/1	0/1	0/1	0/1
p53.129V9	9	ALNKMFCQV	1322	75	165	7.7	15	--	4	4	2/4	0/3	0/2	0/2	0/2
p53.129B7V9	9	ALNKMFBQV	1323	192	391	23	49	--	4	4	2/4	0/3	0/2	0/2	0/2
p53.132	9	KMFQLAKT	1324	333	33	18	106	--	4	4	1/3	0/2	0/2	0/2	0/2
p53.132V9	9	KMFQLAKV	1325	33	8.4	7.7	15	--	4	4	1/3	0/2	0/2	0/2	0/2
p53.132B4V9	9	KMFQBQLAKV	1326	125	13	9.1	37	8889	4	5/5	0/4	0/4	0/4	0/4	0/4
p53.132L2V9	9	KLFQLAKV	1327	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3	0/3	0/3	0/3
p53.139	9	KTCPVQLWV	1328	725	606	217	15	--	2	2	2/5	2/3	1/3	1/3	1/3
p53.139L2	9	KLCPVQLWV	1329	122	239	29	23	--	4	4	3/4	2/3	1/2	1/2	1/2
p53.139L2B3	9	KLBPVQLWV	1330	45	29	19	31	--	4	4	3/4	2/3	1/2	1/2	1/2
p53.149	9	STPPPGRV	1331	909	1162	1031	--	129	1	1	1/1	1/1	1/1	1/1	1/1
p53.149L2	9	SLLPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	0/3	0/3	0/3	0/3
p53.149M2	9	SMPPPGTRV	1333	172	215	13	425	667	4	2/4	2/4	2/4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	--	1	1	1/1	1/1	1/1	1/1	1/1
p53.216L2	10	VLYPYEPPEV	1335	89	391	71	2056	--	3	3	1/1	1/1	1/1	1/1	1/1
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	6667	0	0	1/3	0/3	0/2	0/2	0/2
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	--	4	4	1/3	0/3	0/2	0/2	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		SEQ ID NO:
				Source	Sequence	
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	1338
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV	1339
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1340
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	1341
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	1342
	A2	A*0207	'21.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1343
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	1344
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	1345
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDYNYNKF	1346
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	1347
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	1348
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYYVRR	1349
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	1350
	B7	B*0702	GM3107	A2 signal seq. 5-13 (L7->Y)	APRTLVYL	1351
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL	1352
	B27	B*2705	LG2	R 60s	FRYNGLIHR	1353
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	PPFKYAAAF	1354
	B35	B*3502	TISI	non-natural (B35CON2)	PPFKYAAAF	1355
	B35	B*3503	EHM	non-natural (B35CON2)	PPFKYAAAF	1356
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	1357
	B51		KAS116	non-natural (B35CON2)	PPFKYAAAF	1358
	B53	B*5301	AMAI	non-natural (B35CON2)	PPFKYAAAF	1359
	B54	B*5401	KT3	non-natural (B35CON2)	PPFKYAAAF	1360
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	1361
	Cw6	Cw*0602	'21.221 transfected	non-natural (C6CON1)	YRHDDGNVL	1362
	Cw7	Cw*0702	'21.221 transfected	non-natural (C6CON1)	YRHDDGNVL	1363
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	1364
	K ^b		EL4	VSV NP 52-59	RGYVFQGL	1365
	D ^d		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	1366
	K ^d		P815	non-natural (KdCON1)	KFNPMKTYI	1367

Table XXXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

	P815	HBVs 28-39	IPQSLDSYWTSL	1368	
B. Class II binding assays					
Species	Antigen	Allele	Cell line	Source	
				Radio-labeled peptide sequence	
				SEQ ID NO:	
Human	DR1	DRBI*0101	LG2	HA Y307-319	1369
	DR2	DRBI*1501	L466.1	MBP 88-102Y	1370
	DR2	DRBI*1601	L242.5	non-natural (760.16)	
	DR3	DRBI*0301	MAT	MT 65KD Y3-13	1371
	DR4w4	DRBI*0401	Preiss	non-natural (717.01)	1372
	DR4w10	DRBI*0402	YAR	non-natural (717.10)	1373
	DR4w14	DRBI*0404	BIN 40	non-natural (717.01)	1374
	DR4w15	DRBI*0405	KT3	non-natural (717.01)	1375
	DR7	DRBI*0701	Pitout	Tet. tox. 830-843	1376
	DR8	DRBI*0802	OLL	Tet. tox. 830-843	1377
	DR8	DRBI*0803	LUY	Tet. tox. 830-843	1378
	DR9	DRBI*0901	HID	Tet. tox. 830-843	1379
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	1380
	DR12	DRB1*1201	Herluf	unknown eluted peptide	
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	
	DR51	DRB5*0101	GMI3107 or L416.3	Tet. tox. 830-843	
	DR51	DRB5*0201	L255.1	HA 307-319	
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	
	DR53	DRB4*0101	L257.6	non-natural (717.01)	
	DQ3.1	DQA1*0301/DQB1*0301	PF	non-natural (ROI V)	
Mouse	IA ^b		DB27.4	non-natural (ROI V)	YAHAAHAAHAAHAAHAA
	IA ^d		A20	non-natural (ROI V)	YAHAAHAAHAAHAAHAA
	IA ^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR
	IA ^s		LS102.9	non-natural (ROI V)	YAHAAHAAHAAHAAHAA
	IA ^u		91.7	non-natural (ROI V)	YAHAAHAAHAAHAAHAA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIEKKK
					1385
					1388

Table XXVI. Crossbinding of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	No. A2			
				A*0201 nM	A*0202 nM	A*0203 nM	A*6802 nM
p53.24	9	KLLPENNVL	1396	313	1955	--	1194
p53.25	11	LLPENNVLSPV	1397	19	6.2	4.5	--
p53.65	10	RMPEAAPPVA	1398	78	102	13	1702
p53.65	9	RMPEAAPPV	1399	119	23	22	--
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625
p53.132	9	KMFCQQLAKT	1401	333	33	18	--
p53.135	9	CQLAKTCPV	1402	208	43	143	90
p53.136	8	QLAKTCPV	1403	455	--	100	2643
p53.164	9	KQSQHMTEV	1404	500	130	170	1067
p53.187	11	GLAPPQHLIRV	1405	79	39	11	--
p53.193	11	HILRVEGNLRV	1406	385	1387	83	1194
p53.229	9	CTTHYNYM	1407	278	287	2564	1778
p53.263	10	NLLGRNSFEV	1408	217	--	2500	561
p53.264	9	LLGRNSFEV	1409	85	358	37	181
						881	--
						206	1
						--	4

-- indicates binding affinity = 10,000nM.

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147

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ			A*0201	A*0202	A*0203	A*0206	A*6802	No. A2	CTL	CTL
		ID	nM	nM	nM	nM	nM	nM	Crossbound	Alleles	Wild-type ¹	Tumor
p53.135	CQLAKTCPV	1410	208	43	143	90	-- ²	4	4	1/4	0/1	

1) Number of donors yielding a positive response/total tested.
 2) -- indicates binding affinity = 10,000nM.

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Table XXVIII. Crossbinding of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201			A*0202			A*0203			A*0206			A*6802			No. A2 Alleles	Crossbound
				nM	nM	nM	nM	nM	nM	nM	nM	nM	nM	nM	nM	nM	nM			
p53.69	8	AAPPVAPA	1411	5000	1536	1177	1233	4706	--	--	--	--	--	--	--	--	--	0		
p53.6912V8	8	ALPPVAPV	1412	217	7167	500	285	67	--	--	--	--	--	--	--	--	--	4		
p53.101	11	KTYQGSYGFRL	1413	1786	896	--	--	--	514	615	--	--	--	--	--	--	--	0		
p53.101L2V1	11	KLYQGSYGFRL	1414	81	48	24	116	--	--	--	--	--	--	--	--	--	--	4		
p53.129	9	ALNKMFCQL	1415	735	391	19	73	--	--	--	--	--	--	--	--	--	--	3		
p53.129V9	9	ALNKMFCQV	1416	75	165	7.7	15	--	--	--	--	--	--	--	--	--	--	4		
p53.129BV9	9	ALNKMFBQV	1417	192	391	23	49	--	--	--	--	--	--	--	--	--	--	4		
p53.129	10	ALNKMFCQLA	1418	1316	1075	71	4625	--	--	--	--	--	--	--	--	--	--	1		
p53.129V10	10	ALNKMFCQLV	1419	217	287	71	7400	--	--	--	--	--	--	--	--	--	--	3		
p53.132	9	KMFCQLAKT	1420	333	33	18	106	--	--	--	--	--	--	--	--	--	--	4		
p53.132V9	9	KMFCQLAKV	1421	33	8.4	7.7	15	--	--	--	--	--	--	--	--	--	--	4		
p53.132B4V9	9	KMFBQLAKV	1422	125	13	9.1	37	8889	--	--	--	--	--	--	--	--	--	4		
p53.132L2V9	9	KLFCQLAKV	1423	98	3.6	3.4	10	1270	--	--	--	--	--	--	--	--	--	4		
p53.135	9	CQLAKTCPV	1424	208	43	143	90	--	--	--	--	--	--	--	--	--	--	4		
p53.135L2	9	CLAKAKTCPV	1425	125	506	67	370	--	--	--	--	--	--	--	--	--	--	3		
p53.135B1B7	9	BQLAKTBPV	1426	102	71	15	67	--	--	--	--	--	--	--	--	--	--	4		
p53.135B1L2I	9	BULAKTBPV	1427	46	119	7.7	64	--	--	--	--	--	--	--	--	--	--	4		
p53.139	9	KTCPVQLWV	1428	725	606	217	15	--	--	--	--	--	--	--	--	--	--	2		
p53.139L2	9	KLCPVQLWV	1429	122	239	29	23	--	--	--	--	--	--	--	--	--	--	4		
p53.139L2B3	9	KLBPVQLWV	1430	46	29	19	31	--	--	--	--	--	--	--	--	--	--	4		
p53.149	9	STPPPGBTGV	1431	909	1162	1031	--	129	--	--	--	--	--	--	--	--	--	1		
p53.149M2	9	SMPPPPGBTGV	1432	172	215	13	425	667	--	--	--	--	--	--	--	--	--	4		
p53.149L2	9	SLPPPGBTGV	1433	122	226	13	9250	140	--	--	--	--	--	--	--	--	--	4		
p53.164	9	KQSQHMTEV	1434	500	130	170	285	--	--	--	--	--	--	--	--	--	--	4		
p53.164L2	9	KLSQHMTEV	1435	122	94	35	46	--	--	--	--	--	--	--	--	--	--	4		
p53.216	10	VVVPYEPPEV	1436	617	1870	455	1194	--	--	--	--	--	--	--	--	--	--	1		
p53.216L2	10	VLPVPYEPPEV	1437	89	391	71	2056	--	--	--	--	--	--	--	--	--	--	3		
p53.236	11	YMCNSSCMGGGM	1438	667	391	67	974	5333	--	--	--	--	--	--	--	--	--	2		
p53.236L2M1	11	YLCNSSCMGGGV	1439	22	13	3.6	18	1569	--	--	--	--	--	--	--	--	--	4		
p53.255	11	ITLEDSSGNLL	1440	1563	1265	2857	507	6667	--	--	--	--	--	--	--	--	--	0		
p53.255L2V1	11	ILLEDSSGNLV	1441	33	123	71	206	--	--	--	--	--	--	--	--	--	--	4		

-- indicates binding affinity = 10,000nM.

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Crossbound	CTL Alleles	CTL Peptide ¹	CTL Wild-type	CTL Tumor type
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1233	4706	0				
p53.69L2V8	8	ALPPVAPV	1443	217	7167	500	285	67	4	2/4	1/3	0/3	
p53.129	9	ALNKMFCQL	1444	735	391	19	73	-- ²	3				
p53.129V9	9	ALNKMFCQV	1445	75	165	7.7	15	--	4	0/1			
p53.129B7V9	9	ALNKMFBQV	1446	192	391	23	49	--	4	2/4	0/3	0/2	
p53.132	9	KMFQQLAKT	1447	333	33	18	106	--	4				
p53.132V9	9	KMFQQLAKV	1448	33	8.4	7.7	15	--	4	1/3	0/2	0/2	
p53.132B4V9	9	KMFQQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4	
p53.132L2V9	9	KLFQQLAKV	1450	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3	
p53.139	9	KTCFVQLWV	1451	725	606	217	15	--	2				
p53.139L2	9	KLCFVQLWV	1452	122	239	29	23	--	4	2/5	2/3	1/3	
p53.139L2B3	9	KLBPVQLWV	1453	45	29	19	31	--	4	3/4	2/3	1/2	
p53.149	9	STPPPGTRV	1454	909	1162	1031	--	129	1				
p53.149L2	9	SLPPPGTRV	1455	122	226	13	9250	140	4	2/3	1/3		
p53.149M2	9	SMPPPGTRV	1456	172	215	13	425	667	4	2/4	2/4	2/4	
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	--	1				
p53.216L2	10	VLVPYEPPEV	1458	89	391	71	2056	--	3	1/1	1/1		
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	6667	0				
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	--	4	1/3	0/3	0/2	

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

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Table XXX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFR LGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVQ	1462	P53.130	20	804	167	3
39.0309	2	MGG MNRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity = 10,000nM.

Table XXXI. DR supertype cross-binding

Peptide	Sequence	SEQ ID NO:	Source	DR1	DR4w4	DR7	DR2w2	DR2w2	DR6w1	DR5w1	DR8w2	DR147	Broad Binding (5/8)
				nM	nM	nM	β1 nM	β2 nM	9 nM	1 nM	nM	DR147 Binding	
39.0307	GFRLLGFLHSGTAKSV	1467	p53.1.08	2.6	5.4	89	253	167	76	100	29	3	8
39.0308	LNKMFECQLAKTCPV	1468	p53.1.30	20	804	167	5688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.

Table XXX. DR supertype primary binding

Peptide	DR147		SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross-binding
	Algo	Sum						
39.0307	2	GFR LGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	L N K M F C Q L A K T C P V C	1462	P53.130	20	804	167	3
39.0309	2	M G G M N R R P I L T I I T L	1463	P53.243	--	--	--	0
39.0310	2	R R P I L T I I T L E D S S G	1464	P53.248	5000	4500	--	0
39.0311	2	K R A L P N N T S S S P Q P K	1465	P53.305	--	--	--	0
39.0312	2	D G E Y F T L Q I R G R E R F	1466	P53.324	125	--	--	1

-- indicates binding affinity = 10,000nM.

Table XXXIII. HTL candidate peptides

Peptide	Sequence	SEQ ID Source NO:	DR1 nM	DR4w nM	DR7 nM	DR3 nM	DR2w nM	DR2w β 1 nM	DR2w β 2 nM	DR6w 9 nM	DR5w 1 nM	DR8w nM	DR14 7 Bindin ^g (5/8)	Broad Binding 7 Bindin ^g (5/8)	DR 3 Binder
39.0307	GFRLLGFLHSQTAKS	V1485	53.108	2.6	5.4	89	--	253	167	76	100	29	3	8	0
39.0308	LNKMFQQLAKTCPVQ	1486	53.130	20	804	167	-	5688	541	365	2500	1531	3	5	0

-- indicates binding affinity = 10,000nM